RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/767,308A_

Source: _1 Fw/6_

Date Processed by STIC: _1/13/06_

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: _10/767,308A_ CRF Edit Date: _1/17/06_
Edited by: _AV_

____ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

_J_ Corrected the SEQ ID NO. Sequence numbers edited were:

_8_____

____ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

____ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

____ Inserted mandatory headings/numeric identifiers, specifically:

_____

____ Moved responses to same line as heading/numeric identifier, specifically:

_____

_J_ Other:
Sequence 2 - deleted <2217-<2237 section, since
only 2459 nucleotides were in the sequence, and
since no n's were in the sequence

Revised 09/09/2003

IFW

```
 4 <110> APPLICANT: Kapeller-Libermann, Rosana
 5         White, David
 6         MacBeth, Kyle J.
 8 <120> TITLE OF INVENTION: 2786, A NOVEL HUMAN AMINOPEPTIDASE
10 <130> FILE REFERENCE: MPI99-193CN2M
12 <140> CURRENT APPLICATION NUMBER: US 10/767,308A
13 <141> CURRENT FILING DATE: 2004-01-29
15 <150> PRIOR APPLICATION NUMBER: US 09/443,795
16 <151> PRIOR FILING DATE: 1999-11-19
18 <150> PRIOR APPLICATION NUMBER: US 10/056,253
19 <151> PRIOR FILING DATE: 2002-01-24
21 <160> NUMBER OF SEQ ID NOS: 8
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 650
27 <212> TYPE: PRT
28 <213> ORGANISM: Homo sapiens
30 <400> SEQUENCE: 1
31 Met Ala Ser Gly Glu His Ser Pro Gly Ser Gly Ala Ala Arg Arg Pro
32 1               5                   10                  15
33 Leu His Ser Ala Gln Ala Val Asp Val Ala Ser Ala Ser Asn Phe Arg
34              20                  25                  30
35 Ala Phe Glu Leu Leu His Leu His Leu Asp Leu Arg Ala Glu Phe Gly
36          35                  40                  45
37 Pro Pro Gly Pro Gly Ala Gly Ser Arg Gly Leu Ser Gly Thr Ala Val
38      50                  55                  60
39 Leu Asp Leu Arg Cys Leu Glu Pro Glu Gly Ala Ala Glu Leu Arg Leu
40 65                  70                  75                  80
41 Asp Ser His Pro Cys Leu Glu Val Thr Ala Ala Ala Leu Arg Arg Glu
42              85                  90                  95
43 Arg Pro Gly Ser Glu Glu Pro Pro Ala Glu Pro Val Ser Phe Tyr Thr
44              100                 105                 110
45 Gln Pro Phe Ser His Tyr Gly Gln Ala Leu Cys Val Ser Phe Pro Gln
46          115                 120                 125
47 Pro Cys Arg Ala Ala Glu Arg Leu Gln Val Leu Leu Thr Tyr Arg Val
48      130                 135                 140
49 Gly Glu Gly Pro Gly Val Cys Trp Leu Ala Pro Glu Gln Thr Ala Gly
50 145                 150                 155                 160
51 Lys Lys Lys Pro Phe Val Tyr Thr Gln Gly Gln Ala Val Leu Asn Arg
52              165                 170                 175
53 Ala Phe Phe Pro Cys Phe Asp Thr Pro Ala Val Lys Tyr Lys Tyr Ser
54              180                 185                 190
55 Ala Leu Ile Glu Val Pro Asp Gly Phe Thr Ala Val Met Ser Ala Ser
```

RAW SEQUENCE LISTING   DATE: 01/17/2006
PATENT APPLICATION: US/10/767,308A   TIME: 13:40:54

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\01172006\J767308A.raw

```
56          195               200               205
57 Thr Trp Glu Lys Arg Gly Pro Asn Lys Phe Phe Phe Gln Met Cys Gln
58      210               215               220
59 Pro Ile Pro Ser Tyr Leu Ile Ala Leu Ala Ile Gly Asp Leu Val Ser
60 225               230               235               240
61 Ala Glu Val Gly Pro Arg Ser Arg Val Trp Ala Glu Pro Cys Leu Ile
62               245               250               255
63 Asp Ala Ala Asn Glu Glu Tyr Asn Gly Val Ile Glu Glu Phe Leu Ala
64               260               265               270
65 Thr Gly Glu Lys Leu Phe Gly Pro Tyr Val Trp Gly Arg Tyr Asp Leu
66      275               280               285
67 Leu Phe Met Pro Pro Ser Phe Pro Phe Gly Gly Met Glu Asn Pro Cys
68      290               295               300
69 Leu Thr Phe Val Thr Pro Cys Leu Leu Ala Gly Asp Arg Ser Leu Ala
70 305               310               315               320
71 Asp Val Ile Ile His Glu Ile Ser His Ser Trp Phe Gly Asn Leu Val
72               325               330               335
73 Thr Asn Ala Asn Trp Gly Glu Phe Trp Leu Asn Glu Gly Phe Thr Met
74               340               345               350
75 Tyr Ala Gln Arg Arg Ile Ser Thr Ile Leu Phe Gly Ala Ala Tyr Thr
76      355               360               365
77 Cys Leu Glu Ala Ala Thr Gly Arg Ala Leu Leu Arg Gln His Met Asp
78      370               375               380
79 Ile Thr Gly Glu Glu Asn Pro Leu Asn Lys Leu Arg Val Lys Ile Glu
80 385               390               395               400
81 Pro Gly Val Asp Pro Asp Asp Thr Tyr Asn Glu Thr Pro Tyr Glu Lys
82               405               410               415
83 Gly Phe Cys Phe Val Ser Tyr Leu Ala His Leu Val Gly Asp Gln Asp
84               420               425               430
85 Gln Phe Asp Ser Phe Leu Lys Ala Tyr Val His Glu Phe Lys Phe Arg
86      435               440               445
87 Ser Ile Leu Ala Asp Asp Phe Leu Asp Phe Tyr Leu Glu Tyr Phe Pro
88      450               455               460
89 Glu Leu Lys Lys Lys Arg Val Asp Ile Ile Pro Gly Phe Glu Phe Asp
90 465               470               475               480
91 Arg Trp Leu Asn Thr Pro Gly Trp Pro Pro Tyr Leu Pro Asp Leu Ser
92               485               490               495
93 Pro Gly Asp Ser Leu Met Lys Pro Ala Glu Glu Leu Ala Gln Leu Trp
94               500               505               510
95 Ala Ala Glu Glu Leu Asp Met Lys Ala Ile Glu Ala Val Ala Ile Ser
96      515               520               525
97 Pro Trp Lys Thr Tyr Gln Leu Val Tyr Phe Leu Asp Lys Ile Leu Gln
98      530               535               540
99 Lys Ser Pro Leu Pro Pro Gly Asn Val Lys Lys Leu Gly Asp Thr Tyr
100 545               550               555               560
101 Pro Ser Ile Ser Asn Ala Arg Asn Ala Glu Leu Arg Leu Arg Trp Gly
102               565               570               575
103 Gln Ile Val Leu Lys Asn Asp His Gln Glu Asp Phe Trp Lys Val Lys
104               580               585               590
```

```
105 Glu Phe Leu His Asn Gln Gly Lys Gln Lys Tyr Thr Leu Pro Leu Tyr
106         595                 600                 605
107 His Ala Met Met Gly Gly Ser Glu Val Ala Gln Thr Leu Ala Lys Glu
108         610                 615                 620
109 Thr Phe Ala Ser Thr Ala Ser Gln Leu His Ser Asn Val Val Asn Tyr
110 625                 630                 635                 640
111 Val Gln Gln Ile Val Ala Pro Lys Gly Ser
112                 645                 650
114 <210> SEQ ID NO: 2
115 <211> LENGTH: 2459
116 <212> TYPE: DNA
117 <213> ORGANISM: Homo sapiens
119 <220> FEATURE:
120 <221> NAME/KEY: CDS
121 <222> LOCATION: (62)...(2011)
123 <400> SEQUENCE: 2
124 gcggccgcgt cgacctcccc tcgggttcgc ggcccggccg gtgagcaacg gctctgcggc        60
125 c atg gcg agc ggc gag cat tcc ccc ggc agc ggc gcg gcc cgg cgg ccg        109
126   Met Ala Ser Gly Glu His Ser Pro Gly Ser Gly Ala Ala Arg Arg Pro
127     1               5                   10                  15
129 ctg cac tcc gcg cag gct gtg gac gtg gcc tcg gcc tcc aac ttc cgg        157
130 Leu His Ser Ala Gln Ala Val Asp Val Ala Ser Ala Ser Asn Phe Arg
131             20                  25                  30
133 gcc ttt gag ctg ctg cac ttg cac ctg gac ctg cgg gct gag ttc ggg        205
134 Ala Phe Glu Leu Leu His Leu His Leu Asp Leu Arg Ala Glu Phe Gly
135         35                  40                  45
137 cct cca ggg ccc ggc gca ggg agc cgg ggg ctg agc ggc acc gcg gtc        253
138 Pro Pro Gly Pro Gly Ala Gly Ser Arg Gly Leu Ser Gly Thr Ala Val
139         50                  55                  60
141 ctg gac ctg cgc tgc ctg gag ccc gag ggc gcc gcc gag ctg cgg ctg        301
142 Leu Asp Leu Arg Cys Leu Glu Pro Glu Gly Ala Ala Glu Leu Arg Leu
143 65                  70                  75                  80
145 gac tcg cac ccg tgc ctg gag gtg acg gcg gcg gcg ctg cgg cgg gag        349
146 Asp Ser His Pro Cys Leu Glu Val Thr Ala Ala Ala Leu Arg Arg Glu
147                 85                  90                  95
149 cgg ccc ggc tcg gag gag ccg cct gcg gag ccc gtg agc ttc tac acg        397
150 Arg Pro Gly Ser Glu Glu Pro Pro Ala Glu Pro Val Ser Phe Tyr Thr
151             100                 105                 110
153 cag ccc ttc tcg cac tat ggc cag gcc ctg tgc gtg tcc ttc ccg cag        445
154 Gln Pro Phe Ser His Tyr Gly Gln Ala Leu Cys Val Ser Phe Pro Gln
155         115                 120                 125
157 ccc tgc cgc gcc gcc gag cgc ctc cag gtg ctg ctc acc tac cgc gtc        493
158 Pro Cys Arg Ala Ala Glu Arg Leu Gln Val Leu Leu Thr Tyr Arg Val
159         130                 135                 140
161 ggg gag gga ccc ggg gtt tgc tgg ttg gct ccc gag cag aca gca gga        541
162 Gly Glu Gly Pro Gly Val Cys Trp Leu Ala Pro Glu Gln Thr Ala Gly
163 145                 150                 155                 160
165 aag aag aag ccc ttc gtg tac acc cag ggc cag gct gtc cta aac cgg        589
166 Lys Lys Lys Pro Phe Val Tyr Thr Gln Gly Gln Ala Val Leu Asn Arg
```

RAW SEQUENCE LISTING   DATE: 01/17/2006
PATENT APPLICATION: US/10/767,308A   TIME: 13:40:54

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\01172006\J767308A.raw**

```
167                  165                  170                  175
169 gcc ttc ttc cct tgc ttc gac acg cct gct gtt aaa tac aag tat tca     637
170 Ala Phe Phe Pro Cys Phe Asp Thr Pro Ala Val Lys Tyr Lys Tyr Ser
171                  180                  185                  190
173 gct ctt att gag gtc cca gat ggc ttc aca gct gtg atg agt gct agc     685
174 Ala Leu Ile Glu Val Pro Asp Gly Phe Thr Ala Val Met Ser Ala Ser
175          195                  200                  205
177 acc tgg gag aag aga ggt cca aat aag ttc ttc ttc cag atg tgt cag     733
178 Thr Trp Glu Lys Arg Gly Pro Asn Lys Phe Phe Phe Gln Met Cys Gln
179          210                  215                  220
181 ccc atc ccc tcc tat ctg ata gct ttg gcc atc gga gat ctg gtt tcg     781
182 Pro Ile Pro Ser Tyr Leu Ile Ala Leu Ala Ile Gly Asp Leu Val Ser
183 225                  230                  235                  240
185 gct gaa gtt gga ccc agg agc cgg gtg tgg gct gag ccc tgc ctg att     829
186 Ala Glu Val Gly Pro Arg Ser Arg Val Trp Ala Glu Pro Cys Leu Ile
187          245                  250                  255
189 gat gct gcc aat gag gag tac aac ggg gtg ata gaa gaa ttt ttg gca     877
190 Asp Ala Ala Asn Glu Glu Tyr Asn Gly Val Ile Glu Glu Phe Leu Ala
191          260                  265                  270
193 aca gga gag aag ctt ttt gga cct tat gtt tgg gga agg tat gac ttg     925
194 Thr Gly Glu Lys Leu Phe Gly Pro Tyr Val Trp Gly Arg Tyr Asp Leu
195          275                  280                  285
197 ctc ttc atg cca ccg tcc ttt cca ttt gga gga atg gag aac cct tgt     973
198 Leu Phe Met Pro Pro Ser Phe Pro Phe Gly Gly Met Glu Asn Pro Cys
199          290                  295                  300
201 ctg acc ttt gtc acc ccc tgc ctg cta gct ggg gac cgc tcc ttg gca     1021
202 Leu Thr Phe Val Thr Pro Cys Leu Leu Ala Gly Asp Arg Ser Leu Ala
203 305                  310                  315                  320
205 gat gtc atc atc cat gag atc tcc cac agt tgg ttt ggg aac ctg gtc     1069
206 Asp Val Ile Ile His Glu Ile Ser His Ser Trp Phe Gly Asn Leu Val
207          325                  330                  335
209 acc aac gcc aac tgg ggt gaa ttc tgg ctc aat gaa ggt ttc acc atg     1117
210 Thr Asn Ala Asn Trp Gly Glu Phe Trp Leu Asn Glu Gly Phe Thr Met
211          340                  345                  350
213 tac gcc cag agg agg atc tcc acc atc ctc ttt ggc gct gcg tac acc     1165
214 Tyr Ala Gln Arg Arg Ile Ser Thr Ile Leu Phe Gly Ala Ala Tyr Thr
215          355                  360                  365
217 tgc ttg gag gct gca acg ggg cgg gct ctg ctg cgt caa cac atg gac     1213
218 Cys Leu Glu Ala Ala Thr Gly Arg Ala Leu Leu Arg Gln His Met Asp
219          370                  375                  380
221 atc act gga gag gaa aac cca ctc aac aag ctc cgc gtg aag att gaa     1261
222 Ile Thr Gly Glu Glu Asn Pro Leu Asn Lys Leu Arg Val Lys Ile Glu
223 385                  390                  395                  400
225 cca ggc gtt gac ccg gac gac acc tat aat gag acc ccc tac gag aaa     1309
226 Pro Gly Val Asp Pro Asp Asp Thr Tyr Asn Glu Thr Pro Tyr Glu Lys
227                  405                  410                  415
229 ggt ttc tgc ttt gtc tca tac ctg gcc cac ttg gtg ggt gat cag gat     1357
230 Gly Phe Cys Phe Val Ser Tyr Leu Ala His Leu Val Gly Asp Gln Asp
231                  420                  425                  430
```

```
233 cag ttt gac agt ttt ctc aag gcc tat gtg cat gaa ttc aaa ttc cga    1405
234 Gln Phe Asp Ser Phe Leu Lys Ala Tyr Val His Glu Phe Lys Phe Arg
235         435                 440                 445
237 agc atc tta gcc gat gac ttt ctg gac ttc tac ttg gaa tat ttc cct    1453
238 Ser Ile Leu Ala Asp Asp Phe Leu Asp Phe Tyr Leu Glu Tyr Phe Pro
239     450                 455                 460
241 gag ctt aag aaa aag aga gtg gat atc att cca ggt ttt gag ttt gat    1501
242 Glu Leu Lys Lys Lys Arg Val Asp Ile Ile Pro Gly Phe Glu Phe Asp
243 465                 470                 475                 480
245 cga tgg ctg aat acc ccc ggc tgg ccc ccg tac ctc cct gat ctc tcc    1549
246 Arg Trp Leu Asn Thr Pro Gly Trp Pro Pro Tyr Leu Pro Asp Leu Ser
247                 485                 490                 495
249 cct ggg gac tca ctc atg aag cct gct gaa gag cta gcc caa ctg tgg    1597
250 Pro Gly Asp Ser Leu Met Lys Pro Ala Glu Glu Leu Ala Gln Leu Trp
251         500                 505                 510
253 gca gcc gag gag ctg gac atg aag gcc att gaa gcc gtg gcc atc tct    1645
254 Ala Ala Glu Glu Leu Asp Met Lys Ala Ile Glu Ala Val Ala Ile Ser
255         515                 520                 525
257 ccc tgg aag acc tac cag ctg gtc tac ttc ctg gat aag atc ctc cag    1693
258 Pro Trp Lys Thr Tyr Gln Leu Val Tyr Phe Leu Asp Lys Ile Leu Gln
259     530                 535                 540
261 aaa tcc cct ctc cct cct ggg aat gtg aaa aaa ctt gga gac aca tac    1741
262 Lys Ser Pro Leu Pro Pro Gly Asn Val Lys Lys Leu Gly Asp Thr Tyr
263 545                 550                 555                 560
265 cca agt atc tca aat gcc cgg aat gca gag ctc cgg ctg cga tgg ggc    1789
266 Pro Ser Ile Ser Asn Ala Arg Asn Ala Glu Leu Arg Leu Arg Trp Gly
267                 565                 570                 575
269 caa atc gtc ctt aag aac gac cac cag gaa gat ttc tgg aaa gtg aag    1837
270 Gln Ile Val Leu Lys Asn Asp His Gln Glu Asp Phe Trp Lys Val Lys
271                 580                 585                 590
273 gag ttc ctg cat aac cag ggg aag cag aag tat aca ctt ccg ctg tac    1885
274 Glu Phe Leu His Asn Gln Gly Lys Gln Lys Tyr Thr Leu Pro Leu Tyr
275         595                 600                 605
277 cac gca atg atg ggt ggc agt gag gtg gcc cag acc ctc gcc aag gag    1933
278 His Ala Met Met Gly Gly Ser Glu Val Ala Gln Thr Leu Ala Lys Glu
279     610                 615                 620
281 act ttt gca tcc acc gcc tcc cag ctc cac agc aat gtt gtc aac tat    1981
282 Thr Phe Ala Ser Thr Ala Ser Gln Leu His Ser Asn Val Val Asn Tyr
283 625                 630                 635                 640
285 gtc cag cag atc gtg gca ccc aag ggc agt tagaggctcg tgtgcatggc      2031
286 Val Gln Gln Ile Val Ala Pro Lys Gly Ser
287                 645                 650
289 ccctgcctct tcaggctctc caggctttca gaataattgt ttgttcccaa attcctgttc  2091
290 cctgatcaac ttcctggagt ttatatcccc tcaggataat ctattctcta gcttaggtat  2151
291 ctgtgactct tgggcctctg ctctggtggg aacttacttc tctatagccc actgagcccc  2211
292 gagacagaga acctgcccac agctctcccc gctacaggct gcaggcactg cagggcagcg  2271
293 ggtattctcc tccccaccta agtctctggg aagaagtgga gaggactgat gctcttcttt  2331
294 tttctctttc tgtccttttt cttgctgatt ttatgcaaag ggctggcatt ctgattgttc  2391
295 ttttttcagg tttaatcctt attttaataa agttttcaag caaaaattaa aaaaaaaaaa  2451
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 01/17/2006
PATENT APPLICATION: US/10/767,308A   TIME: 13:40:55

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\01172006\J767308A.raw**

<u>ease Note:</u>
of n and/or Xaa have been detected in the Sequence Listing. Please review the
uence Listing to ensure that a corresponding explanation is presented in the <220>
<223> fields of each sequence which presents at least one n or Xaa.

#:3; Xaa Pos. 27
#:8; Xaa Pos. 3,4,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23

VERIFICATION SUMMARY   DATE: 01/17/2006
PATENT APPLICATION: US/10/767,308A   TIME: 13:40:55

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\01172006\J767308A.raw**

```
306 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
310 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:16
376 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
380 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
384 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:17
```

**Raw Sequence Listing before editing,
for reference only**

RAW SEQUENCE LISTING　　　　　　　DATE: 01/13/2006
PATENT APPLICATION:　**US/10/767,308A**　　TIME: 15:50:06

Input Set : **A:\Sequence listing.txt**
Output Set: **N:\CRF4\01132006\J767308A.raw**

```
 4 <110> APPLICANT: Kapeller-Libermann, Rosana
 5         White, David
 6         MacBeth, Kyle J.
 8 <120> TITLE OF INVENTION: 2786, A NOVEL HUMAN AMINOPEPTIDASE
10 <130> FILE REFERENCE: MPI99-193CN2M
12 <140> CURRENT APPLICATION NUMBER: US 10/767,308A
13 <141> CURRENT FILING DATE: 2004-01-29
15 <150> PRIOR APPLICATION NUMBER: US 09/443,795
16 <151> PRIOR FILING DATE: 1999-11-19
18 <150> PRIOR APPLICATION NUMBER: US 10/056,253
19 <151> PRIOR FILING DATE: 2002-01-24
21 <160> NUMBER OF SEQ ID NOS: 8
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
```

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

see pp 2-3

<210> 8
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Zinc Binding Consensus Sequence

<221> VARIANT
<222> (3)...(4)
<223> Xaa = any amino acid

<221> VARIANT
<222> (6)...(23)
<223> Xaa = any amino acid

<400> ~~8~~ 74 ← replace with

```
His Glu Xaa Xaa His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1               5                   10                  15
Xaa Xaa Xaa Xaa Xaa Xaa Glu
        20
```

```
<210> 2
<211> 2459
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (62)...(2011)

<221> misc_feature
<222> (1)...(3107)
<223> n = A,T,C or G

<400> 2
```

delete because: 1) only 2459 nucleotides in the sequence

2) no n's in the sequence

Input Set : **A:\Sequence listing.txt**
Output Set: **N:\CRF4\01132006\J767308A.raw**

L:127 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:310 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:314 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:16
L:380 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:384 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:388 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:388 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:8 differs:74
L:389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74 after pos.:0
M:341 Repeated in SeqNo=8